

2002-011 seq 1st
SEQUENCE LISTING

<110> AKZO Nobel N.V.

<120> novel Brachyspira hyodysenteriae vaccine

<130> Bhyovaccine

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 1614

<212> DNA

<213> Brachyspira hyodysenteria

<220>

<221> CDS

<222> (1)..(1611)

<223>

<400> 1

atg	aaa	aaa	cta	tat	tca	tta	ttt	ata	ttt	ata	gct	gta	att	tta	ttt	48
Met	Lys	Lys	Leu	Tyr	Ser	Leu	Phe	Ile	Phe	Ile	Ala	Val	Ile	Leu	Phe	
1				5					10					15		

att	tat	tca	tgc	gga	agt	tat	ttt	aat	cct	aaa	tac	tat	ttt	ttt	aaa	96
Ile	Tyr	Ser	Cys	Gly	Ser	Tyr	Phe	Asn	Pro	Lys	Tyr	Tyr	Phe	Phe	Lys	
			20					25					30			

agt	aaa	gta	gag	aat	aat	gga	agt	tct	gga	agc	tca	ggc	ggt	aat	tca	144
Ser	Lys	Val	Glu	Asn	Asn	Gly	Ser	Ser	Gly	Ser	Ser	Gly	Gly	Asn	Ser	
		35				40						45				

gga	ata	tat	ata	cag	cct	ggt	gaa	gat	gaa	gat	cct	ttt	aca	gca	cct	192
Gly	Ile	Tyr	Ile	Gln	Pro	Gly	Glu	Asp	Glu	Asp	Pro	Phe	Thr	Ala	Pro	
	50					55					60					

aaa	tat	gca	tct	gag	tgg	tgg	aat	gat	cct	aat	aat	ggt	gga	ttt	gat	240
Lys	Tyr	Ala	Ser	Glu	Trp	Trp	Asn	Asp	Pro	Asn	Asn	Gly	Gly	Phe	Asp	

65	2002-011 seq 1st										80	
	70					75						
gct tcg gat ata gat aaa tgg ttt ttg aaa gtt gaa ttt tta gca aat	288											
Ala Ser Asp Ile Asp Lys Trp Phe Leu Lys Val Glu Phe Leu Ala Asn												
	85											
	90											
gat tat cca agt tac aga ttt tta aca aaa agc gga aga aaa gca gga	336											
Asp Tyr Pro Ser Tyr Arg Phe Leu Thr Lys Ser Gly Arg Lys Ala Gly												
	100											
	105											
	110											
cat gtt tgg gta gtt tct aat gaa caa tct cag gca tat tta gat caa	384											
His Val Trp Val Val Ser Asn Glu Gln Ser Gln Ala Tyr Leu Asp Gln												
	115											
	120											
	125											
gga gaa gta tgc aat act aca gca gtt acc ggg gta tct ata aaa cca	432											
Gly Glu Val Cys Asn Thr Thr Ala Val Thr Gly Val Ser Ile Lys Pro												
	130											
	135											
	140											
gta gca aat gta aca gga gta aca tat aca aaa tat aag gga ttg aat	480											
Val Ala Asn Val Thr Gly Val Thr Tyr Thr Lys Tyr Lys Gly Leu Asn												
	145											
	150											
	155											
gca aga ttt ttc act cat gac gga gat tat cat aat gta tat cct gga	528											
Ala Arg Phe Phe Thr His Asp Gly Asp Tyr His Asn Val Tyr Pro Gly												
	165											
	170											
	175											
aaa gat aag ata agc aga ttc tat ttt tat tat ttt aca ggt act ccg	576											
Lys Asp Lys Ile Ser Arg Phe Tyr Phe Tyr Tyr Phe Thr Gly Thr Pro												
	180											
	185											
	190											
gaa atg gct aaa ttt tta gaa aat tgc tta ata gct gta gac aca tac	624											
Glu Met Ala Lys Phe Leu Glu Asn Cys Leu Ile Ala Val Asp Thr Tyr												
	195											
	200											
	205											
tca aaa cta tta ttt tac tat gga aga cct caa agc gat tat cca aat	672											
Ser Lys Leu Leu Phe Tyr Tyr Gly Arg Pro Gln Ser Asp Tyr Pro Asn												
	210											
	215											
	220											
cct cca agc tgg cag aag cct agt aat ttg gtt gat aaa tac tct cct	720											
Pro Pro Ser Trp Gln Lys Pro Ser Asn Leu Val Asp Lys Tyr Ser Pro												
	225											
	230											
	235											
aca ggt tat tgg ata tct ata gat gaa ggt ata aat gat aag ggg cag	768											
Thr Gly Tyr Trp Ile Ser Ile Asp Glu Gly Ile Asn Asp Lys Gly Gln												
	245											
	250											
	255											
aat tat cct ttt tat gaa tat gat cct gta gga tat gta aaa agc gat	816											
Asn Tyr Pro Phe Tyr Glu Tyr Asp Pro Val Gly Tyr Val Lys Ser Asp												
	260											
	265											
	270											
ggt aca gtt gtt ata ttt gat tgg ttt gca aac aga tta aga gga aat	864											
Gly Thr Val Val Ile Phe Asp Trp Phe Ala Asn Arg Leu Arg Gly Asn												
	275											
	280											
	285											
cat aat aat gat cct ata aaa agt gat cct aaa gga gct att gtt cct	912											
His Asn Asn Asp Pro Ile Lys Ser Asp Pro Lys Gly Ala Ile Val Pro												
	290											
	295											
	300											
aat cct aat act aat cct tct gct tca act aca gga cgt tct cct tat	960											
Asn Pro Asn Thr Asn Pro Ser Ala Ser Thr Thr Gly Arg Ser Pro Tyr												
	305											
	310											
	315											
	320											
gca ttc tat tcg cct tta gca caa aaa gat aaa act aaa ata act ata	1008											

2002-011 seq 1st

Ala	Phe	Tyr	Ser	Pro	Leu	Ala	Gln	Lys	Asp	Lys	Thr	Lys	Ile	Thr	Ile	
				325					330					335		
agt	act	aca	aaa	tta	ata	aat	tat	aca	gtt	ttc	agt	tat	aaa	tac	agt	1056
Ser	Thr	Thr	Lys	Leu	Ile	Asn	Tyr	Thr	Val	Phe	Ser	Tyr	Lys	Tyr	Ser	
			340					345					350			
ata	caa	ata	ttt	ccg	cct	agt	atg	aaa	gaa	gaa	aaa	ctt	cct	tat	gct	1104
Ile	Gln	Ile	Phe	Pro	Pro	Ser	Met	Lys	Glu	Glu	Lys	Leu	Pro	Tyr	Ala	
			355				360					365				
tat	att	gca	tat	gct	tcc	tat	ggg	gca	gct	tat	caa	aat	gaa	agc	agc	1152
Tyr	Ile	Ala	Tyr	Ala	Ser	Tyr	Gly	Ala	Ala	Tyr	Gln	Asn	Glu	Ser	Ser	
	370					375					380					
aaa	tct	gta	gag	atg	ata	tct	gat	ata	aat	aaa	gga	gag	cat	tac	gga	1200
Lys	Ser	Val	Glu	Met	Ile	Ser	Asp	Ile	Asn	Lys	Gly	Glu	His	Tyr	Gly	
	385				390					395					400	
agt	att	aca	aga	ata	agc	act	gta	cct	aaa	ata	gat	aaa	gac	gga	gga	1248
Ser	Ile	Thr	Arg	Ile	Ser	Thr	Val	Pro	Lys	Ile	Asp	Lys	Asp	Gly	Gly	
				405					410					415		
gag	ttg	gta	aaa	gaa	gga	tct	aag	tct	ttt	gaa	tta	tat	ggg	att	gat	1296
Glu	Leu	Val	Lys	Glu	Gly	Ser	Lys	Ser	Phe	Glu	Leu	Tyr	Gly	Ile	Asp	
			420					425					430			
act	aaa	gat	aca	ttt	ata	gaa	tta	agt	tta	aaa	cta	att	aaa	aat	gat	1344
Thr	Lys	Asp	Thr	Phe	Ile	Glu	Leu	Ser	Leu	Lys	Leu	Ile	Lys	Asn	Asp	
		435					440					445				
gaa	aat	aca	gaa	ttt	gtt	gat	caa	gga	aca	gca	ggg	act	ggg	cct	tta	1392
Glu	Asn	Thr	Glu	Phe	Val	Asp	Gln	Gly	Thr	Ala	Gly	Thr	Gly	Pro	Leu	
	450					455					460					
gta	tac	ttt	gat	aaa	aca	gat	cct	ata	ctt	gta	tta	aaa	tat	gat	aaa	1440
Val	Tyr	Phe	Asp	Lys	Thr	Asp	Pro	Ile	Leu	Val	Leu	Lys	Tyr	Asp	Lys	
	465				470					475					480	
tct	tct	gac	agc	ttc	aaa	tac	agc	agt	gta	aaa	gga	aac	aag	caa	ata	1488
Ser	Ser	Asp	Ser	Phe	Lys	Tyr	Ser	Ser	Val	Lys	Gly	Asn	Lys	Gln	Ile	
				485					490					495		
gaa	gtt	gac	agc	aat	tta	tca	att	aaa	aga	gga	gag	aat	aaa	gag	ttt	1536
Glu	Val	Asp	Ser	Asn	Leu	Ser	Ile	Lys	Arg	Gly	Glu	Asn	Lys	Glu	Phe	
			500					505					510			
aca	gtt	aaa	ttt	aaa	gat	cca	aat	aat	gga	aat	gag	ttt	ggg	gtt	gta	1584
Thr	Val	Lys	Phe	Lys	Asp	Pro	Asn	Asn	Gly	Asn	Glu	Phe	Gly	Val	Val	
		515					520					525				
ttt	aaa	ata	gat	ttt	gaa	aaa	ata	tca	tga							1614
Phe	Lys	Ile	Asp	Phe	Glu	Lys	Ile	Ser								
	530					535										

<210> 2

<211> 537

<212> PRT

<213> Brachyspira hyodysenteria

2002-011 seq 1st

<400> 2

Met Lys Lys Leu Tyr Ser Leu Phe Ile Phe Ile Ala Val Ile Leu Phe
1 5 10 15
Ile Tyr Ser Cys Gly Ser Tyr Phe Asn Pro Lys Tyr Tyr Phe Phe Lys
20 25 30
Ser Lys Val Glu Asn Asn Gly Ser Ser Gly Ser Ser Gly Gly Asn Ser
35 40 45
Gly Ile Tyr Ile Gln Pro Gly Glu Asp Glu Asp Pro Phe Thr Ala Pro
50 55 60
Lys Tyr Ala Ser Glu Trp Trp Asn Asp Pro Asn Asn Gly Gly Phe Asp
65 70 75 80
Ala Ser Asp Ile Asp Lys Trp Phe Leu Lys Val Glu Phe Leu Ala Asn
85 90 95
Asp Tyr Pro Ser Tyr Arg Phe Leu Thr Lys Ser Gly Arg Lys Ala Gly
100 105 110
His Val Trp Val Val Ser Asn Glu Gln Ser Gln Ala Tyr Leu Asp Gln
115 120 125
Gly Glu Val Cys Asn Thr Thr Ala Val Thr Gly Val Ser Ile Lys Pro
130 135 140
Val Ala Asn Val Thr Gly Val Thr Tyr Thr Lys Tyr Lys Gly Leu Asn
145 150 155 160
Ala Arg Phe Phe Thr His Asp Gly Asp Tyr His Asn Val Tyr Pro Gly
165 170 175
Lys Asp Lys Ile Ser Arg Phe Tyr Phe Tyr Tyr Phe Thr Gly Thr Pro
180 185 190
Glu Met Ala Lys Phe Leu Glu Asn Cys Leu Ile Ala Val Asp Thr Tyr
195 200 205
Ser Lys Leu Leu Phe Tyr Tyr Gly Arg Pro Gln Ser Asp Tyr Pro Asn
210 215 220
Pro Pro Ser Trp Gln Lys Pro Ser Asn Leu Val Asp Lys Tyr Ser Pro
225 230 235 240

2002-011 seq 1st

Thr Gly Tyr Trp Ile Ser Ile Asp Glu Gly Ile Asn Asp Lys Gly Gln
245 250 255

Asn Tyr Pro Phe Tyr Glu Tyr Asp Pro Val Gly Tyr Val Lys Ser Asp
260 265 270

Gly Thr Val Val Ile Phe Asp Trp Phe Ala Asn Arg Leu Arg Gly Asn
275 280 285

His Asn Asn Asp Pro Ile Lys Ser Asp Pro Lys Gly Ala Ile Val Pro
290 295 300

Asn Pro Asn Thr Asn Pro Ser Ala Ser Thr Thr Gly Arg Ser Pro Tyr
305 310 315 320

Ala Phe Tyr Ser Pro Leu Ala Gln Lys Asp Lys Thr Lys Ile Thr Ile
325 330 335

Ser Thr Thr Lys Leu Ile Asn Tyr Thr Val Phe Ser Tyr Lys Tyr Ser
340 345 350

Ile Gln Ile Phe Pro Pro Ser Met Lys Glu Glu Lys Leu Pro Tyr Ala
355 360 365

Tyr Ile Ala Tyr Ala Ser Tyr Gly Ala Ala Tyr Gln Asn Glu Ser Ser
370 375 380

Lys Ser Val Glu Met Ile Ser Asp Ile Asn Lys Gly Glu His Tyr Gly
385 390 395 400

Ser Ile Thr Arg Ile Ser Thr Val Pro Lys Ile Asp Lys Asp Gly Gly
405 410 415

Glu Leu Val Lys Glu Gly Ser Lys Ser Phe Glu Leu Tyr Gly Ile Asp
420 425 430

Thr Lys Asp Thr Phe Ile Glu Leu Ser Leu Lys Leu Ile Lys Asn Asp
435 440 445

Glu Asn Thr Glu Phe Val Asp Gln Gly Thr Ala Gly Thr Gly Pro Leu
450 455 460

Val Tyr Phe Asp Lys Thr Asp Pro Ile Leu Val Leu Lys Tyr Asp Lys
465 470 475 480

Ser Ser Asp Ser Phe Lys Tyr Ser Ser Val Lys Gly Asn Lys Gln Ile
Page 5

485 2002-011 seq 1st 495
490

Glu Val Asp Ser Asn Leu Ser Ile Lys Arg Gly Glu Asn Lys Glu Phe
500 505 510

Thr Val Lys Phe Lys Asp Pro Asn Asn Gly Asn Glu Phe Gly Val Val
515 520 525

Phe Lys Ile Asp Phe Glu Lys Ile Ser
530 535

<210> 3

<211> 540

<212> DNA

<213> Brachyspira hyodysenteria

<220>

<221> CDS

<222> (1)..(537)

<223>

<400> 3

atg ttt aag aaa ctt ttt att gtt gtg ggt ttg atg agt gtg ctt gct 48
Met Phe Lys Lys Leu Phe Ile Val Val Gly Leu Met Ser Val Leu Ala
1 5 10 15

gga tgt gaa act atg cag cct aaa aat aat gat aca att gta aaa aat 96
Gly Cys Glu Thr Met Gln Pro Lys Asn Asn Asp Thr Ile Val Lys Asn
20 25 30

gat aat tca tct aat gaa gat aaa aaa gaa gaa act ata act aga gaa 144
Asp Asn Ser Ser Asn Glu Asp Lys Lys Glu Glu Thr Ile Thr Arg Glu
35 40 45

gat aca cca aaa atg aaa gtt aca gtt tat gga gca gat aaa gaa att 192
Asp Thr Pro Lys Met Lys Val Thr Val Tyr Gly Ala Asp Lys Glu Ile
50 55 60

caa gct gtg gaa ata aat gat aaa act tat tat gta ata ggc gga aaa 240
Gln Ala Val Glu Ile Asn Asp Lys Thr Tyr Tyr Val Ile Gly Gly Lys
65 70 75 80

gat gtt gag aat atg aca gaa gct gat ata aaa aaa tca tct tta gta 288
Asp Val Glu Asn Met Thr Glu Ala Asp Ile Lys Lys Ser Ser Leu Val
85 90 95

gca cct tta aaa gtt aca gaa gaa act gtt aat ggt aca aga ggt ata 336
Ala Pro Leu Lys Val Thr Glu Glu Thr Val Asn Gly Thr Arg Gly Ile
100 105 110

2002-011 seq 1st

gtt gtt aca tat tat gat gta aaa gta ttc ttg ggt aaa aga aca gga	384
Val Val Thr Tyr Tyr Asp Val Lys Val Phe Leu Gly Lys Arg Thr Gly	
115 120 125	
aca gga act atc gta gga ata ttc gag cct cag aaa aat gat tgg act	432
Thr Gly Thr Ile Val Gly Ile Phe Glu Pro Gln Lys Asn Asp Trp Thr	
130 135 140	
aca gga aat gat ttg gat aga agt tta tct att caa ata aaa tta tct	480
Thr Gly Asn Asp Leu Asp Arg Ser Leu Ser Ile Gln Ile Lys Leu Ser	
145 150 155 160	
aga aat ata gca ggt cct ata gat ata aaa aga gga agc ata tct tta	528
Arg Asn Ile Ala Gly Pro Ile Asp Ile Lys Arg Gly Ser Ile Ser Leu	
165 170 175	
gca ttt aat taa	540
Ala Phe Asn	

<210> 4

<211> 179

<212> PRT

<213> Brachyspira hyodysenteria

<400> 4

Met Phe Lys Lys Leu Phe Ile Val Val Gly Leu Met Ser Val Leu Ala	
1 5 10 15	
Gly Cys Glu Thr Met Gln Pro Lys Asn Asn Asp Thr Ile Val Lys Asn	
20 25 30	
Asp Asn Ser Ser Asn Glu Asp Lys Lys Glu Glu Thr Ile Thr Arg Glu	
35 40 45	
Asp Thr Pro Lys Met Lys Val Thr Val Tyr Gly Ala Asp Lys Glu Ile	
50 55 60	
Gln Ala Val Glu Ile Asn Asp Lys Thr Tyr Tyr Val Ile Gly Gly Lys	
65 70 75 80	
Asp Val Glu Asn Met Thr Glu Ala Asp Ile Lys Lys Ser Ser Leu Val	
85 90 95	
Ala Pro Leu Lys Val Thr Glu Glu Thr Val Asn Gly Thr Arg Gly Ile	
100 105 110	
Val Val Thr Tyr Tyr Asp Val Lys Val Phe Leu Gly Lys Arg Thr Gly	

2002-011 seq 1st
125

115

120

Thr Gly Thr Ile Val Gly Ile Phe Glu Pro Gln Lys Asn Asp Trp Thr
130 135 140

Thr Gly Asn Asp Leu Asp Arg Ser Leu Ser Ile Gln Ile Lys Leu Ser
145 150 155 160

Arg Asn Ile Ala Gly Pro Ile Asp Ile Lys Arg Gly Ser Ile Ser Leu
165 170 175

Ala Phe Asn